

Abstract**Crystal Structure**

5 A 2.2 Å crystal structure of rabbit AMP deaminase, an integral enzyme of purine nucleotide interconversion, has been determined, in an unligated state and with an inhibitor bound. The present invention further discloses the use of x-ray crystallographic data for identification and construction of possible therapeutic compounds in the treatment of various disease conditions. The sequence of rabbit AMP deaminase is also
10 disclosed.

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